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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/836,077

DATE: 06/26/2001
TIME: 07:54:50

Input Set : A:\00015082.app
Output Set: N:\CRF3\06262001\I836077.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: FLECKENSTEIN, Bernhard
 7 ENSSER, Armin
 9 (ii) TITLE OF INVENTION: HUMAN SEMAPHORIN L (H-SEMAL) AND
 10 CORRESPONDING SEMAPHORINS IN OTHER SPECIES
 12 (iii) NUMBER OF SEQUENCES: 44
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: Frommer Lawrence & Haug LLP
 16 (B) STREET: 745 Fifth Avenue
 17 (C) CITY: New York
 18 (D) STATE: New York
 19 (E) COUNTRY: USA
 20 (F) ZIP: 10151
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 28 (vi) CURRENT APPLICATION DATA:
 29 (A) APPLICATION NUMBER: US/09/836,077
 C--> 30 (B) FILING DATE: 16-Apr-2001
 C--> 31 (C) CLASSIFICATION:
 33 (viii) ATTORNEY/AGENT INFORMATION:
 34 (A) NAME: Lawrence, William F.
 35 (B) REGISTRATION NUMBER: 28,029
 36 (C) REFERENCE/DOCKET NUMBER: 514429-3647
 38 (ix) TELECOMMUNICATION INFORMATION:
 39 (A) TELEPHONE: 212-588-0800
 40 (B) TELEFAX: 212-588-0500
 43 (2) INFORMATION FOR SEQ ID NO: 1:
 45 (i) SEQUENCE CHARACTERISTICS:
 46 (A) LENGTH: 2636 base pairs
 47 (B) TYPE: nucleic acid
 48 (C) STRANDEDNESS: single
 49 (D) TOPOLOGY: linear
 51 (ii) MOLECULE TYPE: DNA (genomic)
 56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 58 CGGGGCCACG GGATGACGCC TCCTCCGCC GGACGTGCCG CCCCCAGCGC ACCGCGCGCC 60
 60 CGCGTCCCTG GCCCGCCGGC TCGGTTGGGG CTTCCGCTGC GGCTGCCGCT GCTGCTGCTG 120
 62 CTCTGGCGG CCGCCGCTC CGCCCAGGGC CACCTAAGGA GCGGACCCCG CATCTCGCC 180
 64 GTCTGGAAAG GCCATGTAGG GCAGGACCGG GTGGACTTTG GCCAGACTGA GCCGCACACG 240
 66 GTGCTTTCC ACGAGCCAGG CAGCTCCTCT GTGTGGGTGG GAGGACGTGG CAAGGTCTAC 300
 68 CTCTTGACT TCCCCGAGGG CAAGAACGCA TCTGTGCGCA CGGTGAATAT CGGCTCCACA 360
 70 AAGGGGTCT GTCTGGATAA GCGGGACTGC GAGAACTACA TCACTCTCCT GGAGAGGCAGG 420
 72 AGTGAGGGC TGCTGGCTG TGGCACCAAC GCCCAGCACC CCAGCTGCTG GAACCTGGTG 480
 74 AATGGCACTG TGGTGCCTACT TGGCGAGATG AGAGGCTACG CCCCCCTTCAG CCCGGACGAG 540

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76	AACTCCCTGG	TTCTGTTGA	AGGGGACGAG	GTGTATTCCA	CCATCCGGAA	GCAGGAATAC	600
78	AATGGGAAGA	TCCCTCGGTT	CCGCCGCATC	CGGGGCGAGA	GTGAGCTGTA	CACCACTGAT	660
80	ACTGTCAATGC	AGAACCCACA	GTTCATCAA	GCCACCATCG	TGCACCAAGA	CCAGGCTTAC	720
82	GATGACAAGA	TCTACTACTT	CTTCCGAGAG	GACAATCCTG	ACAAGAATCC	TGAGGCTCCT	780
84	CTCAATGTGT	CCCGTGTGGC	CCAGTTGTGC	AGGGGGGACC	AGGGTGGGGA	AAGTCACTG	840
86	TCAGTCTCCA	AGTGGAACAC	TTTCTGAAA	GCCATGCTGG	TATGCAGTGA	TGCTGCCACC	900
88	AAACAAGAACT	TCAACAGGCT	GCAAGACGTC	TTCCCTGCTCC	CTGACCCAG	CGGCCAGTGG	960
90	AGGGACACCA	GGGTCTATGG	TGTTTCTCC	AACCCCTGGA	ACTACTCAGC	CGTCTGTGTG	1020
92	TATTCCCTCG	GTGACATTGA	CAAGGTCTTC	CGTACCTCCT	CACTCAAGGG	CTACCACTCA	1080
94	AGCCTTCCCA	ACCCGCGGCC	TGGCAAGTGC	CTCCCAGACC	AGCAGCCGAT	ACCCACAGAG	1140
96	ACCTTCCAGG	TGGCTGACCG	TCACCCAGAG	GTGGCGCAGA	GGGTGGAGCC	CATGGGGCCT	1200
98	CTGAAGACGC	CATTGTTCCA	CTCTAAATAC	CACTACCAGA	AAGTGGCCGT	TCACCGCATG	1260
100	CAAGCCAGCC	ACGGGGAGAC	CTTTCATGTG	CTTTACCTAA	CTACAGACAG	GGGCACTATC	1320
102	CACAAGGTGG	TGGAACCGGG	GGAGCAGGAG	CACAGCTTCG	CCTTCAACAT	CATGGAGATC	1380
104	CAGCCCTTC	GCCGCGCGGC	TGCCATCCAG	ACCATGTCGC	TGGATGCTGA	CGGGAGGAAG	1440
106	CTGTATGTGA	GCTCCCAGTG	GGAGGTGAGC	CAGGTGCC	TGGACCTGTG	TGAGGTCTAT	1500
108	GGCGGGGGCT	GCCACGGTTG	CCTCATGTCC	CGAGACCCCT	ACTGCGGCTG	GGACCAGGGC	1560
110	CGCTGCATCT	CCATCTACAG	CTCCGAACGG	TCAGTGCTGC	AATCCATTAA	TCCAGCCGAG	1620
112	CCACACAAGG	AGTGTCCAA	CCCCAAACCA	GACAAGGCC	CACTGCAGAA	GGTTTCCCTG	1680
114	GCCCCAAACT	CTCGCTACTA	CCTGAGCTGC	CCCATGGAAT	CCCGCCACGC	CACCTACTCA	1740
116	TGGGCCACA	AGGAGAACGT	GGAGCAGAGC	TGCGAACCTG	GTCACCAGAG	CCCCAACTGC	1800
118	ATCCTGTTCA	TCGAGAACCT	CACGGCGCAG	CAGTACGGCC	ACTACTCTG	CGAGGCCCCAG	1860
120	GAGGGCTCCT	ACTTCGCGA	GGCTCAGCAC	TGGCAGCTGC	TGCCCAGGGA	CGGCATCATG	1920
122	GCCGAGCACC	TGCTGGGTCA	TGCCTGTGCC	CTGGCTGCCT	CCCTCTGGCT	GGGGGTGCTG	1980
124	CCCACACTCA	CTCTTGGCTT	GCTGGTCCAC	TAGGGCCTCC	CGAGGCTGGG	CATGCCTCAG	2040
126	GCTTCTGCAG	CCCAGGGCAC	TAGAACGTC	CACACTCAGA	GCCGGCTGGC	CGGGGAGCTC	2100
128	CTTGCCTGCC	ACTTCTTCCA	GGGGACAGAA	TAACCCAGTG	GAGGATGCCA	GGCCTGGAGA	2160
130	CGTCCAGCCG	CAGGGCGCTG	CTGGGCC	GGTGGCGCAC	GGATGGTGAG	GGCTGAGAA	2220
132	TGAGGGCACC	GACTGTGAAG	CTGGGGCATC	GATGACCCAA	GACTTATCT	TCTGGAAAAT	2280
134	ATTTCAGA	CTCCTAAAC	TTGACTAAAT	GCAGCGATGC	TCCCAGCCA	AGAGCCCATG	2340
136	GGTCGGGGAG	TGGGTTGGA	TAGGAGAGCT	GGGACTCCAT	CTCGACCC	GGGCTGAGGC	2400
138	CTGAGTCCTT	CTGGACTCTT	GGTACCCACA	TTGCCTCCTT	CCCCTCC	TCTCATGGCT	2460
140	GGGTGGCTGG	TGTTCTGAA	GACCCAGGGC	TACCCCTCTG	CCAGCCCTGT	CCTCTGCAGC	2520
142	TCCCTCTCTG	GTCCTGGTC	CCACAGGACA	GCCGCC	ATGTTATTG	AAGGATGTTT	2580
144	GCTTCCCGA	CGGAAGGACG	AAAAAAAGCTC	TGAAAAAAA	AAAAAAA	AAAAAA	2636

146 (2) INFORMATION FOR SEQ ID NO: 2:

148 (i) SEQUENCE CHARACTERISTICS:

149 (A) LENGTH: 1195 base pairs

150 (B) TYPE: nucleic acid

151 (C) STRANDEDNESS: single

152 (D) TOPOLOGY: linear

154 (ii) MOLECULE TYPE: DNA (genomic)

159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

161	CGGGGCTGCG	GGATGACGCC	TCCTCCTCCC	GGACGTGCCG	CCCCCAGCGC	ACCGCGCGCC	60
163	CGCGTCCTCA	GCCTGCCGGC	TCGGTTCGGG	CTCCCGCTGC	GGCTGCGGCT	TCTGCTGGTG	120
165	TTCTGGGTGG	CCGCCGCCTC	CGCCCAAGGC	CACTCGAGGA	GGGACCCCG	CATCTCCGCC	180
167	GTCTGGAAAG	GGCAGGACCA	TGTGGACTTT	AGCCAGCCTG	AGCCACACAC	CGTGT	240
169	CATGAGCCGG	GCAGCTTCTC	TGTCTGGGTG	GGTGGACGTG	GCAAGGTCTA	CCACTTCAAC	300
171	TTCCCCGAGG	GCAAGAATGC	CTCTGTGCGC	ACGGTGAACA	TCGGCTCCAC	AAAGGGTCC	360

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173	TGTCAGGACA AACAGGACTG TGGGAATTAC ATCACTCTTC TAGAAAGGCG GGGTAATGGG	420
175	CTGCTGGTCT GTGGCACCAA TGCCCGGAAG CCCAGCTGCT GGAACCTGGT GAATGACAGT	480
177	GTGGTGTATGT CACTTGGTGA GATGAAAGGC TATGCCCT TCAGCCCGA TGAGAACTCC	540
179	CTGGTTCTGT TTGAAGGAGA TGAAGTGTAC TCTACCATCC GGAAGCAGGA ATACAACGGG	600
181	AAGATCCCTC GGTTTCGACG CATTGGGGC GAGAGTGAAC TGTACACAAG TGATACAGTC	660
183	ATGCAGAAC CACAGTTCAT CAAGGCCACC ATTGTGCACC AAGACCAAGC CTATGATGAT	720
185	AAGATCTACT ACTTCTCCG AGAAGACAAAC CCTGACAAGA ACCCCGAGGC TCCTCTCAAT	780
187	GTGTCCCGAG TAGCCCAGTT GTGCAGGGGG GACCAGGGTG GTGAGAGTTC GTTGTCTGTC	840
189	TCCAAGTGGA ACACCTTCCT GAAAGCCATG TTGGTCTGCA GCGATGCAGC CACCAACAGG	900
191	AACCTCAATC GGCTGCAAGA TGTCTTCCTG CTCCCTGACC CCAGTGGCCA GTGGAGAGAT	960
193	ACCAGGGTCT ATGGCGTTT CTCCAACCCC TGGAACTACT CAGCTGCTG CGTGTATTG	1020
195	CTTGGTGACA TTGACAGAGT CTTCCGTACC TCATCGCTCA AAGGCTACCA CATGGGCCTT	1080
197	TCCAACCCCTC GACCTGGCAT GTGCCTCCCA AAAAAGCAGC CCATACCCAC AGAAACCTTC	1140
199	CAGGTAGCTG ATAGTCACCC AGAGGGTGG CAGAGGGTGG AACCTATGGG GCCCC	1195

201 (2) INFORMATION FOR SEQ ID NO: 3:

203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 666 amino acids
205 (B) TYPE: amino acid
W--> 206 (C) STRANDEDNESS: n/a
207 (D) TOPOLOGY: linear

W--> 209 (ii) MOLECULE TYPE: amino acid

214	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
216	Met Thr Pro Pro Pro Pro Gly Arg Ala Ala Pro Ser Ala Pro Arg Ala
217	1 5 10 15
219	Arg Val Pro Gly Pro Pro Ala Arg Leu Gly Leu Pro Leu Arg Leu Arg
220	20 25 30
222	Leu Leu Leu Leu Trp Ala Ala Ala Ser Ala Gln Gly His Leu
223	35 40 45
225	Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln
226	50 55 60
228	Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His
229	65 70 75 80
231	Glu Pro Gly Ser Ser Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr
232	85 90 95
234	Leu Phe Asp Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn
235	100 105 110
237	Ile Gly Ser Thr Lys Gly Ser Cys Leu Asp Lys Arg Asp Cys Glu Asn
238	115 120 125
240	Tyr Ile Thr Leu Leu Glu Arg Arg Ser Glu Gly Leu Leu Ala Cys Gly
241	130 135 140
243	Thr Asn Ala Arg His Pro Ser Cys Trp Asn Leu Val Asn Gly Thr Val
244	145 150 155 160
246	Val Pro Leu Gly Glu Met Arg Gly Tyr Ala Pro Phe Ser Pro Asp Glu
247	165 170 175
249	Asn Ser Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg
250	180 185 190
252	Lys Gln Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly
253	195 200 205
255	Glu Ser Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe

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256	210	215	220
258	Ile Lys Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile		
259	225	230	235
261	Tyr Tyr Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro		240
262	245	250	255
264	Leu Asn Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly		
265	260	265	270
267	Glu Ser Ser Leu Ser Val Ser Lys Trp Asn Thr Phe Leu Lys Ala Met		
268	275	280	285
270	Leu Val Cys Ser Asp Ala Ala Thr Asn Lys Asn Phe Asn Arg Leu Gln		
271	290	295	300
273	Asp Val Phe Leu Leu Pro Asp Pro Ser Gly Gln Trp Arg Asp Thr Arg		
274	305	310	315
276	Val Tyr Gly Val Phe Ser Asn Pro Trp Asn Tyr Ser Ala Val Cys Val		
277	325	330	335
279	Tyr Ser Leu Gly Asp Ile Asp Lys Val Phe Arg Thr Ser Ser Leu Lys		
280	340	345	350
282	Gly Tyr His Ser Ser Leu Pro Asn Pro Arg Pro Gly Lys Cys Leu Pro		
283	355	360	365
285	Asp Gln Gln Pro Ile Pro Thr Glu Thr Phe Gln Val Ala Asp Arg His		
286	370	375	380
288	Pro Glu Val Ala Gln Arg Val Glu Pro Met Gly Pro Leu Lys Thr Pro		
289	385	390	395
291	Leu Phe His Ser Lys Tyr His Tyr Gln Lys Val Ala Val His Arg Met		
292	405	410	415
294	Gln Ala Ser His Gly Glu Thr Phe His Val Leu Tyr Leu Thr Thr Asp		
295	420	425	430
297	Arg Gly Thr Ile His Lys Val Val Glu Pro Gly Glu Gln Glu His Ser		
298	435	440	445
300	Phe Ala Phe Asn Ile Met Glu Ile Gln Pro Phe Arg Arg Ala Ala Ala		
301	450	455	460
303	Ile Gln Thr Met Ser Leu Asp Ala Glu Arg Arg Lys Leu Tyr Val Ser		
304	465	470	475
306	Ser Gln Trp Glu Val Ser Gln Val Pro Leu Asp Leu Cys Glu Val Tyr		
307	485	490	495
309	Gly Gly Gly Cys His Gly Cys Leu Met Ser Arg Asp Pro Tyr Cys Gly		
310	500	505	510
312	Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val		
313	515	520	525
315	Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro		
316	530	535	540
318	Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser		
319	545	550	555
321	Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser		
322	565	570	575
324	Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln		
325	580	585	590
327	Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr		
328	595	600	605

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330 Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala
331 610 615 620
333 Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu
334 625 630 635 640
336 Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu
337 645 650 655
339 Pro Thr Leu Thr Leu Gly Leu Leu Val His
340 660 665

342 (2) INFORMATION FOR SEQ ID NO: 4:

344 (i) SEQUENCE CHARACTERISTICS:
345 (A) LENGTH: 394 amino acids
346 (B) TYPE: amino acid
W--> 347 (C) STRANDEDNESS: n/a
348 (D) TOPOLOGY: linear

W--> 350 (ii) MOLECULE TYPE: amino acid

355 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

357 Met Thr Pro Pro Pro Gly Arg Ala Ala Pro Ser Ala Pro Arg Ala
358 1 5 10 15
360 Arg Val Leu Ser Leu Pro Ala Arg Phe Gly Leu Pro Leu Arg Leu Arg
361 20 25 30
363 Leu Leu Leu Val Phe Trp Val Ala Ala Ala Ser Ala Gln Gly His Ser
364 35 40 45
366 Arg Ser Gly Pro Arg Ile Ser Ala Val Trp Lys Gly Gln Asp His Val
367 50 55 60
369 Asp Phe Ser Gln Pro Glu Pro His Thr Val Leu Phe His Glu Pro Gly
370 65 70 75 80
372 Ser Phe Ser Val Trp Val Gly Arg Gly Lys Val Tyr His Phe Asn
373 85 90 95
375 Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn Ile Gly Ser
376 100 105 110
378 Thr Lys Gly Ser Cys Gln Asp Lys Gln Asp Cys Gly Asn Tyr Ile Thr
379 115 120 125
381 Leu Leu Glu Arg Arg Gly Asn Gly Leu Leu Val Cys Gly Thr Asn Ala
382 130 135 140
384 Arg Lys Pro Ser Cys Trp Asn Leu Val Asn Asp Ser Val Val Met Ser
385 145 150 155 160
387 Leu Gly Glu Met Lys Gly Tyr Ala Pro Phe Ser Pro Asp Glu Asn Ser
388 165 170 175
390 Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg Lys Gln
391 180 185 190
393 Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly Glu Ser
394 195 200 205
396 Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe Ile Lys
397 210 215 220
399 Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile Tyr Tyr
400 225 230 235 240
402 Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro Leu Asn
403 245 250 255
405 Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Glu Ser

VERIFICATION SUMMARY

PATENT APPLICATION: **US/09/836,077**

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Input Set : **A:\00015082.app**

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:206 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=3

L:209 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3

L:347 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=4

L:350 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4